

**BLASTP 2.2.8 [Jan-05-2004]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1079122645-18035-203521758519.BLASTQ3

Query=

(264 letters)

**Database:** All non-redundant GenBank CDS

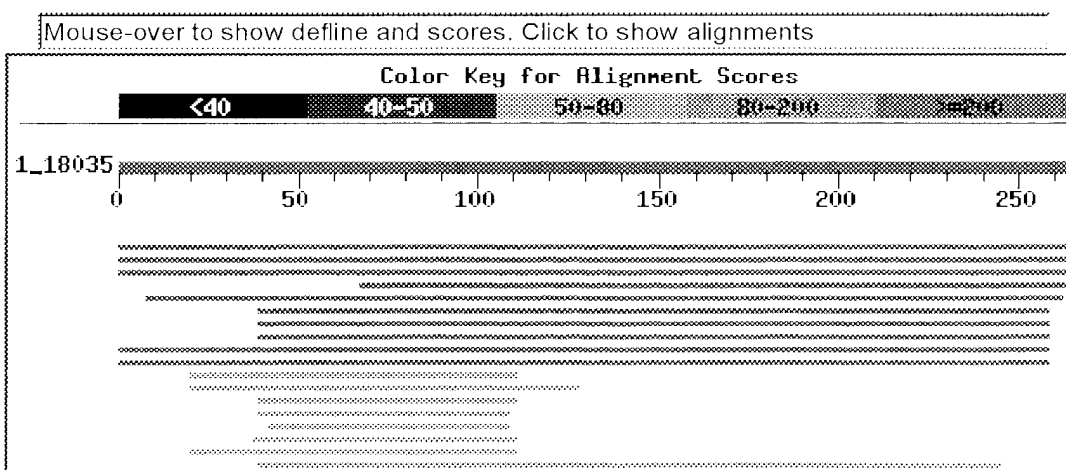
translations+PDB+SwissProt+PIR+PRF

2,678,069 sequences; 748,330,716 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 1058 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E  
(bits) Value

<a href="#">gi 13128972 ref NP_076932.1 </a>	collectin sub-family member 11...	<a href="#">812</a>	0.0	
<a href="#">gi 38049424 ref XP_283054.2 </a>	collectin sub-family member 11...	<a href="#">736</a>	0.0	
<a href="#">gi 34863397 ref XP_345653.1 </a>	similar to hypothetical protei...	<a href="#">719</a>	0.0	

gi 40548420 ref NP_954705.1	collectin sub-family member 11...	609	e-173	
gi 33417124 gb AAH56052.1	Colec11-prov protein [Xenopus la...	569	e-161	
gi 27718901 ref XP_235330.1	similar to collectin liver 1; ...	246	9e-64	
gi 5453619 ref NP_006429.1	collectin sub-family member 10;...	244	4e-63	
gi 37183194 gb AAQ89397.1	COLEC10 [Homo sapiens]	239	1e-61	
gi 27734138 ref NP_775598.1	collectin liver 1; collectin-L...	234	3e-60	
gi 27530341 dbj BAC53954.1	collectin-L1 [Mus musculus]	233	6e-60	
gi 7656989 ref NP_056534.1	collagen, type V, alpha 3 prepr...	79	3e-13	
gi 9453886 dbj BAB03287.1	pro-alpha 1 type V/XI collagen [...]	77	1e-12	
gi 13994280 ref NP_114117.1	Clq and tumor necrosis factor ...	77	1e-12	
gi 13560506 gb AAK30079.1	collagen-like protein B [Strepto...	74	6e-12	
gi 11096157 gb AAG30218.1	collagen-like surface protein [S...	74	6e-12	
gi 11096147 gb AAG30213.1	collagen-like surface protein [S...	74	1e-11	
gi 841122 gb AAA67751.1	putative collagen alpha-2 (XI) cha...	73	1e-11	
gi 6753482 ref NP_034056.1	procollagen, type XI, alpha 2 [...]	73	1e-11	
gi 11096159 gb AAG30219.1	collagen-like surface protein [S...	73	1e-11	
gi 30316381 sp Q64739 CA2B_MOUSE	Collagen alpha 2(XI) chain...	73	1e-11	
gi 34852201 ref XP_215342.2	similar to Collagen alpha 2(XI...	73	1e-11	
gi 43221771 gb EAC76447.1	unknown [environmental sequence]	73	2e-11	
gi 31239123 ref XP_219975.1	ENSANGP00000016783 [Anopheles ...]	72	3e-11	
gi 9632525 ref NP_049519.1	putative tail fiber protein [Ba...	71	5e-11	
gi 29549 emb CAA68698.1	unnamed protein product [Homo sapi...	71	5e-11	
gi 6759903 gb AAF28099.1	alpha 1 (V) collagen [Gallus gallus]	71	5e-11	
gi 28703797 gb AAH47305.1	COL4A1 protein [Homo sapiens]	71	5e-11	
gi 12314281 emb CAC13153.1	bm472K17.2 (collagen type IV al...	71	5e-11	
gi 7656985 ref NP_001836.1	alpha 1 type IV collagen prepro...	71	5e-11	
gi 7649887 dbj BAA94165.1	tail fiber protein [Escherichia ...]	71	5e-11	
gi 19848250 gb VNL99382.1	collagen IV alpha 1 chain [Anoph...	71	5e-11	
gi 225874 prf 1402236A	collagen alpha1(IV)	71	5e-11	
gi 1173848 gb AAB41274.1	type V collagen	71	5e-11	
gi 115313 sp P20908 CA15_HUMAN	Collagen alpha 1(V) chain pr...	71	6e-11	
gi 1360669 pir CGHU1V	collagen alpha 1(V) chain precursor ...	71	6e-11	
gi 16554579 ref NP_000084.2	alpha 1 type V collagen prepro...	71	6e-11	
gi 38014150 gb AAH08760.3	COL5A1 protein [Homo sapiens]	71	6e-11	
gi 6680958 ref NP_031755.1	procollagen, type XI, alpha 1; ...	71	8e-11	
gi 2119157 pir JX0369	collagen alpha 1(XIX) chain precurs...	70	1e-10	
gi 23468285 gb AAH38308.1	Clqtnf7 protein [Mus musculus]	70	1e-10	
gi 8393173 ref NP_058615.1	procollagen, type V, alpha 3; P...	70	1e-10	
gi 34878304 ref XP_223507.2	similar to Clqtnf7 protein [Ra...	70	1e-10	
gi 10281667 ref NP_001849.1	alpha 1 type XIX collagen prec...	70	1e-10	
gi 30425140 ref NP_780634.1	Clq and tumor necrosis factor ...	70	1e-10	
gi 292352 gb AAA36358.1	collagen	70	1e-10	
gi 182387 gb AAA58468.1	fibril-associated collagen	70	1e-10	
gi 624871 dbj BAA07368.1	al(XIX) collagen chain precursor ...	70	1e-10	
gi 44637832 gb EAK65704.1	unknown [environmental sequence]	70	2e-10	
gi 476846 pir A45748	collagen alpha 1(VII) chain - mouse (...)	70	2e-10	
gi 7656987 ref NP_056549.1	procollagen, type V, alpha 1; p...	70	2e-10	
gi 283868 pir S28791	collagen alpha 1(XI) chain - chicken ...	70	2e-10	
gi 6680972 ref NP_031764.1	procollagen, type VII, alpha 1 ...	70	2e-10	

gi 34859869 ref XP_342327.1	procollagen type XI alpha 1 [R...	69	2e-10	
gi 30354436 gb AAH52161.1	Procollagen, type XI, alpha 1 [M...	69	2e-10	
gi 11120710 ref NP_068528.1	collagen, type V, alpha 3; pro...	69	2e-10	
gi 115347 sp P27393 CA24_ASCSU	Collagen alpha 2(IV) chain p...	69	2e-10	
gi 3172000 emb CAA06511.1	collagen alpha 1 (XI) [Rattus no...	69	2e-10	
gi 11096145 gb AAG30212.1	collagen-like surface protein [S...	69	2e-10	
gi 115328 sp P20909 CA1B_RAT	COLLAGEN ALPHA 1(XI) CHAIN >gi...	69	2e-10	
gi 29566025 ref NP_817595.1	gp4 [Mycobacteriophage Bxz2] >...	69	3e-10	
gi 30145696 emb CAD89749.1	C. elegans COL-135 protein (cor...	69	3e-10	
gi 11096151 gb AAG30215.1	collagen-like surface protein [S...	69	4e-10	
gi 423283 pir  S33603	surfactant protein D - bovine	69	4e-10	
gi 4502961 ref NP_000085.1	alpha 1 type VII collagen precu...	69	4e-10	
gi 44173973 gb EAA52456.1	unknown [environmental sequence]	69	4e-10	
gi 2137076 pir  I48103	type VII collagen - Chinese hamster ...	69	4e-10	
gi 31217994 ref XP_316546.1	ENSANGP00000010005 [Anopheles ...	69	5e-10	
gi 37722541 gb AAO06817.1	asymmetric acetylcholinesterase ...	68	7e-10	
gi 37722545 gb AAO06819.1	asymmetric acetylcholinesterase ...	68	7e-10	
gi 7239359 gb AAF43197.1	acetylcholinesterase collagen-lik...	68	7e-10	
gi 18105030 ref NP_536805.1	acetylcholinesterase collagen-...	68	7e-10	
gi 180715 gb AAA52034.1	alpha-2 type XI collagen	68	7e-10	
gi 18201917 ref NP_542411.1	alpha 2 type XI collagen isofo...	68	7e-10	
gi 1360671 pir  CGHU2E	collagen alpha 2(XI) chain precursor...	68	7e-10	
gi 1000747 gb AAC50215.1	Pro-a2(XI)	68	7e-10	
gi 18201919 ref NP_542412.1	alpha 2 type XI collagen isofo...	68	7e-10	
gi 37722539 gb AAO06816.1	asymmetric acetylcholinesterase ...	68	7e-10	
gi 18105022 ref NP_536801.1	acetylcholinesterase collagen-...	68	7e-10	
gi 18105028 ref NP_536804.1	acetylcholinesterase collagen-...	68	7e-10	
gi 12643942 sp Q9Y215 COLQ_HUMAN	Acetylcholinesterase colla...	68	7e-10	
gi 13432104 sp P13942 CA2B_HUMAN	Collagen alpha 2(XI) chain...	68	7e-10	
gi 3820987 emb CAA20240.1	dJ1033B10.12 (collagen, type XI,...	68	7e-10	
gi 18201915 ref NP_542410.1	alpha 2 type XI collagen isofo...	68	7e-10	
gi 1000746 gb AAC50214.1	Pro-a2(XI) >gi 1584719 prf  21233...	68	7e-10	
gi 37722543 gb AAO06818.1	asymmetric acetylcholinesterase ...	68	7e-10	
gi 18105024 ref NP_536802.1	acetylcholinesterase collagen-...	68	7e-10	
gi 1000745 gb AAC50213.1	Pro-a2(XI)	68	7e-10	
gi 18105016 ref NP_005668.2	acetylcholinesterase collagen-...	68	7e-10	
gi 18105018 ref NP_536799.1	acetylcholinesterase collagen-...	68	7e-10	
gi 18105020 ref NP_536800.1	acetylcholinesterase collagen-...	68	7e-10	
gi 11875612 gb AAG40729.1	type IV collagen alpha 1 chain p...	67	9e-10	
gi 18780273 ref NP_110447.2	alpha 1 type XXI collagen prec...	67	9e-10	
gi 19745166 ref NP_604447.1	collagen, type V, alpha 1 [Rat...	67	9e-10	
gi 6165881 gb AAF04724.1	collagen type XI alpha-1 [Homo sa...	67	9e-10	
gi 18375522 ref NP_542197.1	alpha 1 type XI collagen isofo...	67	9e-10	
gi 6165882 gb AAF04725.1	collagen type XI alpha-1 isoform ...	67	9e-10	
gi 7441219 pir  S18803	collagen alpha 1(V) chain - hamster	67	9e-10	
gi 18375518 ref NP_001845.2	alpha 1 type XI collagen isofo...	67	9e-10	
gi 1360670 pir  CGHU1E	collagen alpha 1(XI) chain precursor...	67	9e-10	
gi 33149359 gb AAO64414.1	type VII collagen [Canis familia...	67	9e-10	

## Alignments

Get selected sequences

Select all

Deselect all

☒ >gi|13128972|ref|NP\_076932.1| ☒ collectin sub-family member 11 isoform a [Homo s  
 gi|12652661|gb|AAH00078.1| ☒ Collectin sub-family member 11 [Homo sapiens]  
 gi|37182003|gb|AAQ88805.1| ☒ RGNL596 [Homo sapiens]  
 Length = 271

Score = 812 bits (1907), Expect = 0.0

Identities = 262/271 (96%), Positives = 262/271 (96%), Gaps = 7/271 (2%)

Query: 1 MRGNLALVGVLI SLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60  
 MRGNLALVGVLI SLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR  
 Sbjct: 1 MRGNLALVGVLI SLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60

Query: 61 VGPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR- 119  
 VGPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR  
 Sbjct: 61 VGPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRK 120

Query: 120 -IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP 178  
 IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP  
 Sbjct: 121 AIGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP 180

Query: 179 KDE-MNGL---GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEE 233  
 KDE NGL YLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN RSGEPNNAYDEE  
 Sbjct: 181 KDEAANGLMAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEE 240

Query: 234 DCVEMVASGGWNDVACHTTMYFMCEFDKENM 264  
 DCVEMVASGGWNDVACHTTMYFMCEFDKENM  
 Sbjct: 241 DCVEMVASGGWNDVACHTTMYFMCEFDKENM 271

☒ >gi|38049424|ref|XP\_283054.2| ☒ collectin sub-family member 11 [Mus musculus]  
 gi|12833584|dbj|BAB22581.1| ☒ unnamed protein product [Mus musculus]  
 Length = 272

Score = 736 bits (1728), Expect = 0.0

Identities = 242/271 (89%), Positives = 253/271 (93%), Gaps = 8/271 (2%)

Query: 1 MRGNLALVGVLI SLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60  
 MR +LAL G+LISLAFLSLLPSG PQ +DACSVQILVPGLKGDAGEKGDKGAPGRPGR  
 Sbjct: 3 MR-DIALAGMLISLAFLSLLPSGCPQQTEDACSVQILVPGLKGDAGEKGDKGAPGRPGR 61

Query: 61 VGPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR- 119  
 VGPTGEKGDMDKGQKG+VGRHGKIGPIG+KGEKGDSDIGPPGP+GEPG+PCECSQLR  
 Sbjct: 62 VGPTGEKGDMDKGQKGTVGRHGKIGPIGAKGEKGDSDIGPPGPSGEPGIPCECSQLRK 121

Query: 120 -IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP 178  
 IGEMDNQV+QLT+ELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQ RGGTLSMP  
 Sbjct: 122 AIGEMDNQVTLTTELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQARGGTLSMP 181

Query: 179 KDE-MNGL--GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEE 233  
 KDE NGL YLAQAGLARVFIGINDLEKEGAFVYSD SPM+TFN RSGEPNNAYDEE

Sbjct: 182 KDEAANGLMASYLAQAAGLARVFIGINDLEKEGAFVYSDRSPMQTFNKWRSGEPPNNAYDEE 241

Query: 234 DCVEMVASGGWNDVACHTTMYFMCEFDKENM 264

DCVEMVASGGWNDVACH TMYFMCEFDKEN+

Sbjct: 242 DCVEMVASGGWNDVACHITMYFMCEFDKENL 272

>gi|34863397|ref|XP\_345653.1| similar to hypothetical protein MGC3279 similar  
[Rattus norvegicus]  
Length = 319

Score = 719 bits (1689), Expect = 0.0

Identities = 239/282 (84%), Positives = 254/282 (90%), Gaps = 19/282 (6%)

Query: 1 MRGNLALVGVLLISLAFLSLLPSGHPQAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60

MR +LAL G+LISLAFLSLLPSG PQ +DACSVQILVPGLKGD+GEKG+KGAPGRPGR

Sbjct: 39 MR-DLALAGMLISLAFLSLLPSGCPQQTEDACSVQILVPGLKGDSEKGNKGAPGRPGR 97

Query: 61 VGPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEIP----- 109

VGPTGEKGDMDKGQKG+VGRHGKIGPIG+KGEKGDSDIGPPGP+GEP

Sbjct: 98 VGPTGEKGDMDKGQKGTVGRHGKIGPIGAKGEKGDSDIGPPGPSGEPASPMNRLHT 157

Query: 110 GLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLS 167

G+PCECSQLR IGEMDNQV+QLT+E+KFIKNAVAGVRETESKIYLLVKEEKRYADAQLS

Sbjct: 158 GIPCECSQLRKAIGEMDNQVTLTTEIKFIKNAVAGVRETESKIYLLVKEEKRYADAQLS 217

Query: 168 CQGRGGTSLMPKDE-MNGL--GYLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--R 222

CQGRGGTSLMPKDE NGL YLAQAAGLARVFIGINDLE+EGAFVYSD SPM+TFN R

Sbjct: 218 CQGRGGTSLMPKDEAANGLMASYLAQAAGLARVFIGINDLEREGAFVYSDRSPMQTFNKWR 277

Query: 223 SGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEFDKENM 264

SGEPNNAYDEEDCVEMVASGGWNDVACH TMYFMCEFDKEN+

Sbjct: 278 SGEPNNAYDEEDCVEMVASGGWNDVACHITMYFMCEFDKENL 319

>gi|40548420|ref|NP\_954705.1| collectin sub-family member 11 isoform b [Homo s  
gi|31455215|gb|AAH09951.1| Collectin sub-family member 11, isoform b [Homo sapi  
Length = 268

Score = 609 bits (1429), Expect = e-173

Identities = 195/204 (95%), Positives = 195/204 (95%), Gaps = 7/204 (3%)

Query: 68 GDMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR--IGEMDN 125

GDMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR IGEMDN

Sbjct: 65 GDMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGEMDN 124

Query: 126 QVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDE-MNG 184

QVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDE NG

Sbjct: 125 QVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDEAANG 184

Query: 185 L--GYLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEEDCVEMVA 240

L YLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFN RSGEPNNAYDEEDCVEMVA

Sbjct: 185 LMAAYLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVA 244

Query: 241 SGGWNDVACHTTMYFMCEFDKENM 264

SGGWNDVACHTTMYFMCEFDKENM

Sbjct: 245 SGGWNDVACHTTMYFMCEFDKENM 268

>gi|33417124|gb|AAH56052.1| Colec11-prov protein [Xenopus laevis]  
Length = 271

Score = 569 bits (1336), Expect = e-161  
Identities = 201/262 (76%), Positives = 223/262 (85%), Gaps = 7/262 (2%)

Query: 9 GVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVGPTEGKG 68  
G +ISL FL LL SG+ Q D+ CSVQILVPGLKGDAGEKG+KGAPGRPGRVGP GEKG  
Sbjct: 9 GTIISLGFLILLGSGYQCQHITDETCSVQILVPGLKGDAGEKGEKGAPGRPGRVGPPEGKG 68

Query: 69 DMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR--IGEMDNQ 126  
++GDKG KGS+GRHGKIGPIGSKGEKGD G IGPPGPNGEPG+PCEC QLR +GEMD Q  
Sbjct: 69 EIGDKGIKGSMDRHHGKIGPIGSKGEKGDVGQIGPPGPNGEPGIPCECQQLRKAVGEMDIQ 128

Query: 127 VSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDE-MNGL 185  
V+QL +E+KF+KN VAGVRETE+KIYLLVKEEK+Y DAQ CQGRGGTLSMPKDE N L  
Sbjct: 129 VAQLATEVKFVKNVAVGRETETKIYLLVKEEKYIDAQDYCQGRGGTLSMPKDEATNSL 188

Query: 186 --GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEEDCVEMVAS 241  
Y+ AGL+RVFIGINDLE+EG FVYSD SPM+TFN R EPNNAYDEEDC EMV+S  
Sbjct: 189 IASYINHAGLSRVFIGINDLEREGHFVYSDRSPMQTFNKWRQAEPPNNAYDEEDCAEMVSS 248

Query: 242 GGWNDVACHTTMYFMCEFDKEN 263  
GGWNDV+C TMYF+CEFDKEN  
Sbjct: 249 GGWNDVSCITMYFICEFDKEN 270

>gi|27718901|ref|XP\_235330.1| similar to collectin liver 1; collectin-L1 [Ratt  
Length = 277

Score = 246 bits (574), Expect = 9e-64  
Identities = 118/231 (51%), Positives = 167/231 (72%), Gaps = 15/231 (6%)

Query: 40 PGLKGDAGEKGDKGAPGRPGRVG---PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGD 96  
PG KGD GE+GD G G+ G+VG P G KG++GD G +G +G K GPIG KG+KG+  
Sbjct: 46 PGPKGDNGERGDTGEEGKDGKVGROGPKGVKGELGDMGAQGDIG--KSGPIGKKGDKGE 102

Query: 97 SGDIGPPGPNGEPGLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLL 154  
G +G PG G+ G C+C + R +G++D V++L + +KFIKN +AG+RETE K Y +  
Sbjct: 103 KGLLGVPGEKGKAGTICDCGRYRKVVQQLDISVARLKTSMKF1KNVIAGIRETEEFYII 162

Query: 155 VKEEKRYADAQLS-CQGRGGTLSMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFV 210  
V+EEK Y ++ L+ C+ RGG L+MPKDE+ N L Y+A++G RVFIG+NDLEKEG +V  
Sbjct: 163 VQFEKNYRES-LTHCRIRGGMIAMPKDEVVNTLIADYVAKSGFFRVFIGVNDLEKEGQYV 221

Query: 211 YSDHSPMRTFN--RSGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259  
++D++P++ ++ + GEP++ Y EDCVEM++SG WND CH TMYF+CEF  
Sbjct: 222 FTDNTPLQNYSNWKEGEPSPDPYGHEDCVEMISSGRWNDTECHLTMYFVCEF 272

>gi|5453619|ref|NP\_006429.1| collectin sub-family member 10; collectin liver 1  
[Homo sapiens]

gi|5162875|dbj|EAA81747.1| collectin 34 [Homo sapiens]  
Length = 277

Score = 244 bits (569), Expect = 4e-63

Identities = 116/231 (50%), Positives = 167/231 (72%), Gaps = 15/231 (6%)

Query: 40 PGLKGDAGEKGDGKAPGRPGRVG---PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGD 96  
 PG KGD GEKGD G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+

Sbjct: 46 PGPKGDDGEKGDPEEGEKHGKVGVRMGPKGIKGLGDMGDRGNIG---KTGP1GKKGDKGE 102

Query: 97 SGD1GPPPGPNGEPGLPCECSQLR--IGEMDNQVSQ1TSELKFIKNAVAGVRETESKIYLL 154  
 G +G PG G+ G C+C + R +G++D +++L + +KF+KN +AG+RETE K Y +



Sbjct: 103 KGLLGIPGEKKGAGTVCDGGRYRK1VVGQLDISIARLK1TSMK1VKNVIAGIRETEEFY1I 162

Query: 155 VKEEKRYADAQ1S-CQGRGGT1SMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFV 210  
 V+EEK Y ++ L+ C+ RGG L+MPKDE N L Y+A++G RVFIG+NDLE+EG ++

Sbjct: 163 VQEEKNYRES-LTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYM 221

Query: 211 YSDHSPMR1F-NRS-GE1PN1AYDEEDCVEMVASGGW1NDVACHTTMYFMCEF 259  
 ++D++P++ + N + GE1P++ Y EDCVEM++SG WND CH TMYF+CEF

Sbjct: 222 FTDN1PLQ1NYSNWNEGEPSDPYGHEDCVEM1SSGRW1NDTECHLTMYFVCEF 272

 >gi|37183194|gb|AA089397.1|  COLEC10 [Homo sapiens]

Length = 277

Score = 239 bits (557), Expect = 1e-61

Identities = 116/231 (50%), Positives = 166/231 (71%), Gaps = 15/231 (6%)

Query: 40 PGLKGDAGEKGDGKAPGRPGRVG---PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGD 96  
 PG KGD GEKGD G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+

Sbjct: 46 PGPKGDDGEKGDPEEGEKHGKVGVRMGPKGIKGLGDMGDQGNIG---KTGP1GKKGDKGE 102

Query: 97 SGD1GPPPGPNGEPGLPCECSQLR--IGEMDNQVSQ1TSELKFIKNAVAGVRETESKIYLL 154  
 G +G PG G+ G C+C + R +G++D +++L + +KF+KN +AG+RETE K Y +

Sbjct: 103 KGLLGIPGEKKGAGTVCDGGRYRK1VVGQLDISIARLK1TSMK1VKNVIAGIRETEEFY1I 162



Query: 155 VKEEKRYADAQ1S-CQGRGGT1SMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFV 210  
 V+EEK Y ++ L+ C+ RGG L+MPKDE N L Y+A++G RVFIG+NDLE+EG ++

Sbjct: 163 VQEEKNYRES-LTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYM 221

Query: 211 YSDHSPMR1F-NRS-GE1PN1AYDEEDCVEMVASGGW1NDVACHTTMYFMCEF 259  
 +D++P++ + N + GE1P++ Y EDCVEM++SG WND CH TMYF+CEF

Sbjct: 222 STDNTPLQ1NYSNWNEGEPSDPYGHEDCVEM1SSGRW1NDTECHLTMYFVCEF 272

 >gi|277341381|ref|NP\_775598.1|  collectin liver 1; collectin-L1 [Mus musculus]

 gi|26324374|gb|EAC25941.1|  unnamed protein product [Mus musculus]

Length = 277

Score = 234 bits (546), Expect = 3e-60

Identities = 128/280 (45%), Positives = 185/280 (66%), Gaps = 36/280 (12%)

Query: 1 MRGNLA--LVGV1ISLAF1SL1PSGHPQPAG---D-----DACSVQ1LVPLKGDAGEKG 50  
 +R NL+ LV L+LL H Q G D + C+ + PG KGD GE+G

Sbjct: 8 LRSNLSMLLV-----LALL---HFQSLGLD1VDSRSAAEVCATHT1SPGPKGDDGERG 56

Query: 51 DKGAPGRPGRVG---PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDG1GPPPGPNG 107  
 D G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+ G +G PG G

Sbjct: 57 DTGEEGKDGKVGQRQGPQKGVKGE LGDMGAQGNIG---KSGPIGKKGDKGEKGLLGIPGEKG 113

Query: 108 EPGLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQ 165  
+ G C+C + R +G++D V++L + +KFIKN +AG+RETE K Y +V+EEK Y ++



Sbjct: 114 KAGTICDCGRYRKVVGQLDISVARLKTSMKFIKNVIAGIRETEEEKFYIYVQEEKNYRES- 172

Query: 166 LS-CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN 221  
L+ C+ RGG L+MPKDE+ N L Y+A++G RVEFIG+NDLE+EG +V++D++P++ ++

Sbjct: 173 LTHCRIRGGMLAMPKDEVVNTLIADYVAKSGFFRVFIGVNDLEREGQYVFTDNTPLQNYNS 232

Query: 222 --RSGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259  
+ EP++ EDCVEM++SG WND CH TMYF+CEF

Sbjct: 233 NWKEEPPSDPSGHEDCVEMLSGRWNDTECHLTMYFVCEF 272

 >gi|27530341|dbj|BAC53954.1|  collectin-L1 [Mus musculus]  
Length = 277

Score = 233 bits (544), Expect = 6e-60  
Identities = 127/278 (45%), Positives = 185/278 (66%), Gaps = 32/278 (11%)

Query: 1 MRGNLALVGVLI SLAFLSLLPSGHPQFAG---D-----DACSVQILVPLKGDAGEKGD 52  
+R NL++ L L+LL H Q G D + C+ + PG KGD GE+GD

Sbjct: 8 LRSNLMS-----LLLLALL---HFQSLGLDVSRSAAEVCATHTISPGPKGDDGERGDT 58

Query: 53 GAPGRPGRVG---PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDGDI GPPGPNGEF 109  
G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+ G +G PG G+

Sbjct: 59 GEEGKDGKVGQRQGPQKGVKGE LGDMGAQGNIG---KSGPIGKKGDKGEKGLLGIPGEKGKA 115

Query: 110 GLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLS 167  
G C+C + R +G++D V++J + +KFIKN +AG+RETE K Y +V+EEK Y ++ L+



Sbjct: 116 GTICDCGRYRKVVGQLDISVARLKTSMKFIKNVIAGIRETEEEKFYIYVQEEKNYRES-LT 174



Query: 168 -CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN-- 221  
C+ RGG L+MPKDE+ N L Y+A++G RVEFIG+NDLE+EG +V++D++P++ ++

Sbjct: 175 HCRIRGGMLAMPKDEVVNTLIADYVAKSGFFRVFIGVNDLEREGQYVFTDNTPLQNYNSW 234

Query: 222 RSGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259  
+ EP++ EDCVEM++SG WND CH TMYF+CEF

Sbjct: 235 KEEPPSDPSGHEDCVEMLSGRWNDTECHLTMYFVCEF 272

 >gi|7656989|ref|NP\_056534.1|  collagen, type V, alpha 3 preproprotein; pro-(alp  
[Homo sapiens]

gi|34223720|sp|P25940|CA35 HUMAN  Collagen alpha 3(V) chain precursor  
gi|7329074|gb|AAF59902.1|  collagen type V alpha 3 chain [Homo sapiens]  
Length = 1745

Score = 78.7 bits (178), Expect = 3e-13  
Identities = 48/92 (52%), Positives = 53/92 (57%), Gaps = 24/92 (26%)

Query: 39 VPGLKGDAGEKGDGK---APGRPGRVGPTGEKGMGDKGQKGSVGR---HGKIGP----- 87  
+PG KGD GEKGD G A G PG+ GP GE D G KGSVG G +GP

Sbjct: 1221 IPGPKGDIGEKD SGPSGAAGPPGKKGPPGE-----D-GAKGSVGPTGI PGDLGPPGDPG 1274

Query: 88 ---I-GSKGEKGDSDGI---GPPGPNGEPLP 112  
I GS GEKGD GD+ GPPG +GEPPG P



Sbjct: 1275 VSGIDGSPGEKGDPGDVGGPGPPGASGEPGAP 1306

Score = 59.6 bits (133), Expect = 2e-07

Identities = 46/117 (39%), Positives = 50/117 (42%), Gaps = 51/117 (43%)

Query: 47 GEKGDKGAPG-----R--PGRVGP-----TGE----- 66  
GEKG KG PG R PGRVGP GE  
Sbjct: 1325 GEKGAKGEPGPDGPPGRTPGPMGARGPPGRVGPGLRGIPGPVGEPPGLLGAPGQMGPPL 1384  
Query: 67 -----KGDMDKGQKGSVGRHGKIGPIGSKGEKGD)SG--DI-GPPGPNGEPGLP 112  
KGD G KG+KG +G G IGP G GEKGD G + GPPGP G+PG P  
Sbjct: 1385 GPSGLPGLKGDTPGKGEKGHIGLIGLIGPPGEAGEKGDQGLPGVQGPFGPKGDPGPP 1441

Score = 55.4 bits (123), Expect = 3e-06

Identities = 42/109 (38%), Positives = 46/109 (42%), Gaps = 48/109 (44%)

Query: 40 PGLKGD-----AGEKGD-----KGAPGRPGRV----- 61  
PGLKGD AGEKGD KG PG PG +  
Sbjct: 1390 PGLKGDTPGKGEKGHIGLIGLIGPPGEAGEKGDQGLPGVQGPFGPKGDPGPPPGPICSLGH 1449  
Query: 62 -GPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGD)SGDIGPPGPNGEP 109  
GP G G +G KG KGS P GS G +GD+G GPPGP G P  
Sbjct: 1450 PGPPGVAGPLGQKGSKGS-----P-GSMGPRGDTGPAGPPGPPGAP 1489

Score = 54.9 bits (122), Expect = 4e-06

Identities = 50/129 (38%), Positives = 59/129 (45%), Gaps = 50/129 (38%)

Query: 21 PSGHPPQAGDDACSVQILV-----PGL----KGDAGEKGDK-----GAPGRPGRVGPPTGEK 67  
P+GHP P G D Q PGL KGD) G +G G PG G GP GEK  
Sbjct: 1107 PAGHPGPPGADG--AQ---GRRGPPGLFGQKGD)GVVRG--FVGVIGPPGLQGLPGPPGEK 1159  
Query: 68 GDMGDKGQKGSVGRHGKIGP-----IGSKGEKGD)SGDIGPP 103  
G++GD G S+G HG GP +G KGE+GD+GD P  
Sbjct: 1160 GEVGDVG---SMGPHGAPGPRGPQGPTGSEGT)PGLPGGVGQPGAVGEKGERGDAGD---P 1213  
Query: 104 GPNGEPGLP 112  
GP G PG+P  
Sbjct: 1214 GPPGAPGIP 1222

Score = 53.7 bits (119), Expect = 1e-05

Identities = 41/92 (44%), Positives = 46/92 (50%), Gaps = 28/92 (30%)

Query: 44 GDAGEKGDK-----GAPGRPGR-----VGPTGEKGDMDKGQKGSVG-RHGKIG 86  
G AGEKG K G PGRPG +GP GEKG G GQ G G R G  
Sbjct: 779 GSAGEKG-KLGVPLPGYPGRPGPKSIGFPGLPIGEKKGKSGKTGQPGLEGER----G 833  
Query: 87 PIGSKGEKGD)SGDIGPPGPNGE-----PGLP 112  
P GS+GE+G G G PGP G+ PG+P  
Sbjct: 834 PPGSRGERGQPGATGQPGPKGDVGDGAPGIP 865

Score = 53.2 bits (118), Expect = 1e-05  
Identities = 35/79 (44%), Positives = 39/79 (49%), Gaps = 27/79 (34%)

Query: 40 PGLKGDAGEKGDKGAPGRPGRVGPTEGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDNSGD 99  
PG KGD G KGD+G PG PG P GE D GP G KG+ G +G+  
Sbjct: 736 PGFKGDVGLKGDQKPGAPG---PRGE-----D-----GPEGPKGQAGQAGE 774  
  
Query: 100 IGPPGPNGE-----PGLP 112  
GPPG GE PGLP  
Sbjct: 775 EGPPGSAGEKKGKLGVPGLP 793

Score = 50.3 bits (111), Expect = 1e-04  
Identities = 43/104 (41%), Positives = 50/104 (48%), Gaps = 36/104 (34%)

Query: 40 PGLKGDAGEKGDKGA-----P-GRPGRVG-----P--TGEKGMG----- 71  
PGLKG+ G +G +G P G PGRVG P TG KGD G  
Sbjct: 499 PGLKGEEGAEGPQGPRLQGPHPGRVGMGRPGADGARGLPGLDTPGPKGDRGFDGLPGL 558  
  
Query: 72 --DKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPN---GEPG 110  
+KGQ+G G G+ GP GE G+ G GPPGP GEPG  
Sbjct: 559 PGEKGQRGDFGHVGPQGP---PGEDGERGAEGPPGPTGQAGEPG 599

Score = 49.4 bits (109), Expect = 2e-04  
Identities = 39/94 (41%), Positives = 50/94 (53%), Gaps = 26/94 (27%)

Query: 40 PGLKGDAGE-----KGDKGAPGRPGRVGPTEG-----EKGMGDKGQKGSVGRHG 83  
PG KGD G+ G+ GAPG PG+ GP+G E G+ G KG+ G G G  
Sbjct: 1282 PGEKGDVGGPVPASGEPEGAPGPPGKRGPSGHMREGRE-GEKGAKGEPGPDGPPG 1340  
  
Query: 84 KIGPIGSKGKGDSDIGP-----PGPNGEPL 111  
+ GP+G++G G +GP PGP GEPGL  
Sbjct: 1341 RTGPMGARGP---PGRVGPGLRGPVGPVGPGL 1371

Score = 47.7 bits (105), Expect = 7e-04  
Identities = 31/63 (49%), Positives = 33/63 (52%), Gaps = 18/63 (28%)

Query: 56 GRPGRVGPTEGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPP-----GPNGEP 109  
G PG GP+GE+GD GD VG P G KG KGD GD GPP GP G P  
Sbjct: 1064 GPPGAAGPSGEEGDKD-----VG-----AP-GHKGSKGD)KGDAGPPGQPGIRGPAGHP 1111  
  
Query: 110 GLP 112  
G P  
Sbjct: 1112 GPP 1114

Score = 46.0 bits (101), Expect = 0.002  
Identities = 44/127 (34%), Positives = 54/127 (42%), Gaps = 58/127 (45%)

Query: 40 PGLKGDAGE-----KGDKGAPG-----R-----PGR-----VGPTGE 66  
PG KG G+ KGDKG PG R PG+ VGP G+  
Sbjct: 979 PGPKGGPDGPPTGLKGDGPPGPGVANGSPGERGPLGPAGGIGLPQGSGSEGPVGPAGK 1038  
  
Query: 67 KGMGDKGQKGSVGRHGKI-GPIG-----SKGEKGDSDIGPP----- 103